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PCT09

RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/830,433A

TIME: 14:08:31

Input Set : A:\09-830,433.Seq.Listing.txt

Output Set: N:\CRF3\02262002\I830433A.raw

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3 <110> APPLICANT: AUJAME et al.
6 <120> TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
7   strains of the Neisseria genius
9 <130> FILE REFERENCE: P07180US00/BAS
11 <140> CURRENT APPLICATION NUMBER: 09/830,433A
12 <141> CURRENT FILING DATE: 2001-04-26
14 <150> PRIOR APPLICATION NUMBER: FR 98 13 693
15 <151> PRIOR FILING DATE: 1998-10-30
17 <160> NUMBER OF SEQ ID NOS: 129
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 858
23 <212> TYPE: DNA
24 <213> ORGANISM: Neisseria meningitidis
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(855)
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33   1           5           10           15
35 cat ttg ggt gta aag atg tat tcg cac act gtt cct gcg att gcc gag   96
36 His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
37           20           25           30
39 ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg   144
40 Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
41           35           40           45
43 tta ttc gat aaa ccg gag cat aaa atc gtt atc aaa gat aat ggt ata   192
44 Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
45           50           55           60
47 gga atg agc ttc gat gaa atc aat gat ttt tat ttg aga atc ggt cgg   240
48 Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
49 65           70           75           80
51 aac aga agg gaa gaa aaa caa gct tcc ccg tgc gga aga att cca acg   288
52 Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
53           85           90           95
55 ggt aaa aaa ggc ctt ggt aaa ttg gca tta ttc ggg ctt ggc aac aaa   336
56 Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Gly Leu Gly Asn Lys
57           100          105          110
59 att gaa att tct act atc cag gga aac gaa agg gtt act ttt act ttg   384
60 Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
61           115          120          125
63 gat tat gca gag att cga aga agc aag ggt att tat caa ccg gag ttt   432

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64 Asp Tyr Ala Glu Ile Arg Arg Ser Lys Gly Ile Tyr Gln Pro Glu Phe
65      130                      135                      140
67 cga aaa gaa tct gtt gaa tcc aat atc gaa agc ggg aca acc ata act 480
68 Arg Lys Glu Ser Val Glu Ser Asn Ile Glu Ser Gly Thr Thr Ile Thr
69 145                      150                      155                      160
71 tta acc gaa ctg acg aaa aag caa gga tat ccg tta gat aat tat gta 528
72 Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
73      165                      170                      175
75 gag cat ctt tcc cgc ttg ttt gat ttt ccg gct cag gat ttt aaa atc 576
76 Glu His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
77      180                      185                      190
79 aaa gta agc ttg aac ggc tct gaa cct aaa atc att gat gga aat cta 624
80 Lys Val Ser Leu Asn Gly Ser Glu Pro Lys Ile Ile Asp Gly Asn Leu
81      195                      200                      205
83 aaa tat gat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat tta 672
84 Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
85      210                      215                      220
87 gca acc aat att tca tcg tta tct tca aaa ttc gaa cag tat gaa tac 720
88 Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
89 225                      230                      235                      240
91 agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768
92 Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
93      245                      250                      255
95 aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816
96 Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
97      260                      265                      270
99 atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa 858
100 Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
101      275                      280                      285
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 285
106 <212> TYPE: PRT
107 <213> ORGANISM: Neisseria meningitidis
109 <400> SEQUENCE: 2
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111 1 5 10 15
113 His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
114 20 25 30
116 Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
117 35 40 45
119 Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
120 50 55 60
122 Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
123 65 70 75 80
125 Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
126 85 90 95
128 Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Gly Leu Gly Asn Lys
129 100 105 110
131 Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu

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132          115          120          125
134 Asp Tyr Ala Glu Ile Arg Arg Ser Lys Gly Ile Tyr Gln Pro Glu Phe
135          130          135          140
137 Arg Lys Glu Ser Val Glu Ser Asn Ile Glu Ser Gly Thr Thr Ile Thr
138 145          150          155          160
140 Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
141          165          170          175
143 Glu His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
144          180          185          190
146 Lys Val Ser Leu Asn Gly Ser Glu Pro Lys Ile Ile Asp Gly Asn Leu
147          195          200          205
149 Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
150          210          215          220
152 Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
153 225          230          235          240
155 Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
156          245          250          255
158 Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
159          260          265          270
161 Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
162          275          280          285
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178 1 5 10 15
180 gac aaa tta cta acc gaa aat acc cat att tgg cta ttt ata ggt gta 96
181 Asp Lys Leu Leu Thr Glu Asn Thr His Ile Trp Leu Phe Ile Gly Val
182 20 25 30
184 tta cac aaa atg tta cct att agt ctg gtg caa tcc cta cta cgt ttc 144
185 Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe
186 35 40 45
188 ggc gaa cgt gtc cat ctt gtc cag tta caa aaa acg ggg aaa aac gca 192
189 Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala
190 50 55 60
192 ttg gat ttt tac ctg tcc tat tac ctc gga caa att acc gcc aca gac 240
193 Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp
194 65 70 75 80
196 ccc aat gcc caa atc ggc ata ctc tcg cgt gat gga gga tac gat gtt 288
197 Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val
198 85 90 95
200 ctg gtc gaa cat att ttg aaa aac cac cag gcg aag ggt atc gtg cgc 336
201 Leu Val Glu His Ile Leu Lys Asn His Gln Ala Lys Gly Ile Val Arg

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202		100		105		110		
204	cta gcc aat	ata gat gaa gta	caa cat cag aaa	att gct acc gaa ccg	384			
205	Leu Ala Asn	Ile Asp Glu Val	Gln His Gln Lys	Ile Ala Thr Glu Pro				
206		115		120		125		
208	ccg tca gca	ttg ctg gaa aac	act cct cag cct	gaa acc acc ctc aaa	432			
209	Pro Ser Ala	Leu Leu Glu Asn	Thr Pro Gln Pro	Glu Thr Thr Leu Lys				
210		130		135		140		
212	cca cag caa	cca tta act tcc	tat ttc caa gca	gcc cta act gca ctg	480			
213	Pro Gln Gln	Pro Leu Thr Ser	Tyr Phe Gln Ala	Leu Thr Ala Leu				
214	145		150		155		160	
216	cgc cgc ccc	gac gct ttc cgc	ccc tgc cgc ctg	cat aac ctg cga caa	528			
217	Arg Arg Pro	Asp Ala Phe Arg	Pro Cys Arg Leu	His Asn Leu Arg Gln				
218		165		170		175		
220	aat ctg cgt	aag cat att ttg	agt gat ttg ttt	aaa gaa aaa acc	gat	576		
221	Asn Leu Arg	Lys His Ile Leu	Ser Asp Leu Phe	Lys Glu Lys Thr	Asp			
222		180		185		190		
224	gaa gaa tgc	gaa ata acc act	gct aac gtt atc	aat aaa ctc aaa	gca	624		
225	Glu Glu Cys	Glu Ile Thr Thr	Ala Asn Val Ile	Asn Lys Leu Lys	Ala			
226		195		200		205		
228	caa aac ttc	atc agc att gat	gaa cag gaa acc	gtt tcc tac cat	ctc	672		
229	Gln Asn Phe	Ile Ser Ile Asp	Glu Gln Glu Thr	Val Ser Tyr His	Leu			
230		210		215		220		
232	agt gat aat	gat ttg tta caa	aga atc caa cgc	cat att tta agc	caa	720		
233	Ser Asp Asn	Asp Leu Leu Gln	Arg Ile Gln Arg	His Ile Leu Ser	Gln			
234	225		230		235		240	
236	cgt ccc aaa	acc tac gct gat	ttt caa gcc gtc	gtg caa aac cga	gca	768		
237	Arg Pro Lys	Thr Tyr Ala Asp	Phe Gln Ala Val	Val Gln Asn Arg	Ala			
238		245		250		255		
240	gat gca ctt	cac tta aca gtc	ggt acc aac gac	att caa tcc ttt	gcg	816		
241	Asp Ala Leu	His Leu Thr Val	Gly Thr Asn Asp	Ile Gln Ser Phe	Ala			
242		260		265		270		
244	cga cat ttg	cgc gac caa aac	ctg atc cgc caa	aac aat ggg aaa	att	864		
245	Arg His Leu	Arg Asp Gln Asn	Leu Ile Arg Gln	Asn Asn Gly Lys	Ile			
246		275		280		285		
248	gaa tat gca	ccg ttt act gaa	cct aaa cca cag	cca acg ccc aag	cag	912		
249	Glu Tyr Ala	Pro Phe Thr Glu	Pro Lys Pro Gln	Pro Thr Pro Lys	Gln			
250		290		295		300		
252	cct aaa aaa	acc gca tgg gaa	cct gat gaa att	att tgg aaa aaa	gtg	960		
253	Pro Lys Lys	Thr Ala Trp Glu	Pro Asp Glu Ile	Ile Trp Lys Lys	Val			
254	305		310		315		320	
256	att gcc gcg	tta tcg tta aag	aac cgt cct aat	aaa acc aaa act	tta	1008		
257	Ile Ala Ala	Leu Ser Leu Lys	Asn Arg Pro Asn	Lys Thr Lys Thr	Leu			
258		325		330		335		
260	cgc aat aca	atc cag gca ctc	aca aaa tcc aat	gca caa gaa act	gac	1056		
261	Arg Asn Thr	Ile Gln Ala Leu	Thr Lys Ser Asn	Ala Gln Glu Thr	Asp			
262		340		345		350		
264	aaa ctg cta	caa cat tta caa	gat gac cca agt	cct acg tat tga		1101		
265	Lys Leu Leu	Gln His Leu Gln	Asp Asp Pro Ser	Pro Thr Tyr				
266		355		360		365		

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269 <210> SEQ ID NO: 4
270 <211> LENGTH: 366
271 <212> TYPE: PRT
272 <213> ORGANISM: Neisseria meningitidis
274 <400> SEQUENCE: 4
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278 Asp Lys Leu Leu Thr Glu Asn Thr His Ile Trp Leu Phe Ile Gly Val
279 20 25 30
281 Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe
282 35 40 45
284 Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala
285 50 55 60
287 Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp
288 65 70 75 80
290 Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val
291 85 90 95
293 Leu Val Glu His Ile Leu Lys Asn His Gln Ala Lys Gly Ile Val Arg
294 100 105 110
296 Leu Ala Asn Ile Asp Glu Val Gln His Gln Lys Ile Ala Thr Glu Pro
297 115 120 125
299 Pro Ser Ala Leu Leu Glu Asn Thr Pro Gln Pro Glu Thr Thr Leu Lys
300 130 135 140
302 Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu
303 145 150 155 160
305 Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln
306 165 170 175
308 Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp
309 180 185 190
311 Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala
312 195 200 205
314 Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu
315 210 215 220
317 Ser Asp Asn Asp Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln
318 225 230 235 240
320 Arg Pro Lys Thr Tyr Ala Asp Phe Gln Ala Val Val Gln Asn Arg Ala
321 245 250 255
323 Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala
324 260 265 270
326 Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile
327 275 280 285
329 Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln
330 290 295 300
332 Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val
333 305 310 315 320
335 Ile Ala Ala Leu Ser Leu Lys Asn Arg Pro Asn Lys Thr Lys Thr Leu
336 325 330 335
338 Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp
339 340 345 350

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VERIFICATION SUMMARY

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Input Set : A:\09-830,433.Seq.Listing.txt

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